In the Claims

Please amend Claims 23, 25, 26, 33 and 59. Amendments to the claims are indicated in the attached "Marked Up Version of Amendments" (pages i - iv).

23. (Amended) A method for identifying genes that carry one or more harmful alleles, comprising:

D1

a) identifying one or more inherited point mutations that are found in one or more genes or portions thereof of a population of young individuals, determining the frequency with which each point mutation occurs, and calculating the sum of the frequencies of all point mutations identified for each gene or segment;

b) identifying one or more inherited point mutations that are found in one or more genes or portions thereof of a population of aged individuals, determining the frequency with which each point mutation occurs, and calculating the sum of the frequencies of all point mutations identified for each gene or segment;

c) comparing the sum of the frequencies of point mutations that are found in a selected gene or portion thereof of the young population calculated in a) with the sum of the frequencies of point mutations that are found in the same gene or portion thereof of the aged population calculated in b),

wherein a significant decrease in the sum of the frequencies of point mutations in the aged population indicates that said selected gene carries one or more harmful alleles.

25. (Twice Amended) A method for identifying genes that carry a harmful allele, comprising:

D2

a) identifying the set of inherited point mutations that are found in one or more genes or portions thereof of a population of young individuals, wherein the set comprises all inherited point mutations occurring at a frequency at about or above 5×10^{-5}, and determining the frequency with which each point mutation occurs;

b) identifying the set of inherited point mutations that are found in the genes or portions thereof of a population of aged individuals, and determining the frequency with which each point mutation occurs; and

D2 cont.

c) comparing the frequency of each point mutation identified in a selected gene or portion thereof of the young population determined in a) with the frequency of the same point mutations identified in said selected gene of the aged population determined in b), wherein a significant decrease in the frequency of two or more point mutations in said selected gene of the aged population relative to said selected gene of the young population indicates that said selected gene carries a harmful allele.

26. (Amended)The method of Claim 25 further comprising:

D3

d) determining the frequency of said two or more point mutations that decrease in the aged population in said selected gene of one or more intermediate age-specific populations;

e) determining the age-specific decrease of said two or more point mutations; and

f) comparing the age-specific decrease in frequency determined in e) with the expected age-specific decrease in frequency of a set of harmful alleles that cause a particular mortal diseases, and determining if the functions are significantly different,

wherein a determination that the age-specific decrease in frequency determined in e) is not significantly different from the expected age-specific decrease in frequency of harmful alleles further indicates that said selected gene carries a harmful allele and has a high probability of being causal of said one or more mortal diseases.

33. (Twice Amended) A method for identifying genes that carry a harmful allele or that are linked to a gene that carries a harmful allele, comprising:

D4

a) identifying the set of inherited point mutations that are found in one or more genes or portions thereof of a population of young individuals, wherein the set comprises all inherited point mutations occurring at a frequency at about or above 5×10^{-5}, and determining the frequency with which each point mutation occurs;

b) identifying the set of inherited point mutations that are found in the genes or portions thereof of a population of aged individuals, and determining the frequency with which each point mutation occurs;

c) comparing the frequency of each point mutation identified in a selected gene or portion thereof of the young population determined in a) with the frequency of the same point mutations identified in said selected gene of the aged population determined in b), wherein a significant decrease in the frequency of a point mutation in said selected gene of the aged population relative to said selected gene of the young population indicates that said selected gene carries a harmful allele or is linked to a gene that carries a harmful allele.

59. (Amended) A method of identifying one or more inherited point mutations in any target region of a genome of a population, wherein said point mutations cause or accelerate the appearance of a mortal disease or prevent or delay the appearance of a mortal disease, comprising:

D5

a) determining the set of all inherited point mutations occurring at a frequency at or above 5×10^{-5} separately in members of the same population that comprises subpopulations selected from the group consisting of young, aged, intermediate age, afflicted with disease, afflicted with a disease of early age onset and afflicted with a disease of late age onset; and

b) determining the frequencies of each inherited point mutation within and between the subpopulations,

wherein a decrease in the frequency in the aged population is indicative of an allele that causes or accelerates a mortal disease, and an increase in frequency in the intermediate or

D5 Cont.

aged population is indicative of an allele that prevents or delays the appearance of a mortal disease.

Please add new Claims 61-65.

61. (NEW) A method of identifying one or more inherited point mutations in any target region of a genome of a population, wherein the point mutations interfere with reproduction, comprising:

a) determining the set of all inherited point mutations occurring at a frequency at or above 5×10^{-5} separately in members of the same population that comprises subpopulations selected from the group consisting of young, aged, intermediate age, afflicted with disease, afflicted with a disease of early age onset and afflicted with a disease of late age onset;

D6

b) determining the frequencies of each inherited point mutation within and between the subpopulations; and

c) determining the point mutations that are obligatory knockout point mutations, wherein a sum frequency of all obligatory knockout point mutations of about 0.02% to about 2% indicates that the gene carries a recessive allele that interferes with reproduction, and a sum frequency of all obligatory knock-out point mutations of less than about 0.02% indicates that said gene carries a dominant allele that interferes with reproduction.

62. (NEW) A method for identifying genes that carry one or more harmful alleles, comprising:

a) identifying one or more inherited point mutations that are found in one or more genes or portions thereof of a population of young individuals, determining the frequency with which each point mutation occurs, and calculating the sum of the frequencies of all point mutations identified for each gene or segment;

b) identifying one or more inherited point mutations that are found in one or more genes or portions thereof of a population of aged individuals, determining the frequency with which each point mutation occurs, and calculating the sum of the frequencies of all point mutations identified for each gene or segment;

c) determining the point mutations that are obligatory knockout point mutations; and

d) comparing the sum of the frequencies of obligatory knockout mutations that are found in a selected gene or portion thereof of the young population calculated in a) with the sum of the frequencies of point mutations that are found in the same gene or portion thereof of the aged population calculated in b),

wherein a significant decrease in the sum of the frequencies of point mutations in the aged population indicates that said selected gene carries one or more harmful alleles.

63. (NEW) The method of Claim 61, wherein a sum frequency of less than about 2% is indicative that the gene carries a deleterious allele.

64. (NEW) The method of Claim 61, wherein a sum frequence greater than about 0.2% but less than about 2% indicates the gene carries a recessive deleterious allele.

65. (NEW) The method of Claim 61, wherein a sum frequency less than about 0.2% indicates the gene carries a dominant deleterious allele.